

Figure 1

[illegible]

MRATSLIAAA LAVAGDALAG KIKYLGVAIP GIDFGCDIDG SCPTDTSSVP LLSYKGGDGA GQMKHFAEDD
10 20 30 40 50 60 70
GLNVFRISAT WQFVLNNTVD GKLDLNLWGS YNKVVNACLE TGAYCMIDMH NFARYNGGII GQGGVSDDIF
80 90 100 110 120 130 140
VDLWVQIAKY YEDNDKIIFG LMNEPHDLDI EIWAQTCQKV VTAIRKAGAT SQMILLPGTN FASVETYVST
150 160 170 180 190 200 210
GSAEALGKIT NPDGSTDLLY FDVHKYLDIN NSGSHAECTT DNVDAFNDAF DWLRQNKRQA IISSETGASME
220 230 240 250 260 270 280
PSCMTAFCAQ NKAISENSDV YIGFVGWAG SFDTSYILTL TPLGKPGNYT DNKLMNECIL DQFTLDEKYR
290 300 310 320 330 340 350
PTPTSISTAA EETATATATS DGDAPSTTKP IFREETASPT PNAVTKPSPD TSDSSDDDDKD SAASMSAQQGL
360 370 380 390 400 410 420
TGTVLFTVAA LGYMLVAF
430 438

Figure 2
Predicted T. reesei EG VIII amino acid sequence